Amendments to the Specification

Please replace the specification at page 1, after the title, as amended on January 27, 2004 with the following paragraph:

This present application is a Continuation of allowed U.S. Application Serial No. 08/942,596 filed October 2, 1997, which is incorporated by reference in its entirety.

Please replace the paragraph at page 17, lines 8-10, which was amended on January 27, 2004, with the following paragraph:

Figure 2A-C. Consensus Nucleic Acid Sequence encoding the open reading frame of the HMW protein from *C. trachoamtis* LGV L_2 (SEQ ID NO.: 1).

Please replace the paragraph at page 17, line 34 to page 18, line 8, as amended on January 27, 2004, with the following paragraph:

Figure 6A-B. Predicted amino acid sequences of HMW Protein for *C. trachomatis* L_2, B, and F. The *C. trachomatis* L_2 sequence (SEQ ID NO: 43) is given in the top line and begins with the first residue of the mature protein, E (see amino acid residues 29-1012 of SEQ ID NO: 2). Potential eucaryotic N-glycosylation sequences are underlined. A hydrophobic helical region flanked by proline rich segments and of suitable length to span the lipid bilayer is underlined and enclosed in brackets. Amino acid differences identified in the B (see amino acid residues 29-1013 of SEQ ID NO: 15) and F (see amino acid residues 29-1013 of SEQ

ID NO: 16) serovars are designated below the L_2 HMWP protein sequence.

Please replace the paragraph at page 18, lines 9-11 with the following paragraph:

Figure 7A-B. Indirect florescence antibody staining of *C. trachomatis* N11 (serovar F) inclusion bodies using anti-rHMWP' antibody.

Please replace the paragraph at page 28, lines 1-13 with the following paragraph:

The nucleotide sequences encoding the HMW protein of the present invention are useful for their ability to selectively form duplex molecules with complementary stretches of other protein genes. Depending on the application, a variety of hybridization conditions may be employed to achieve varying sequence identities. In specific aspects, nucleic acids are provided which comprise a sequence complementary to at least 10, 15, 25, 50, 100, 200 or 250 nucleotides of the HMW protein gene (Figure 2A-C). In specific embodiments, nucleic acids which hybridize to an HMW protein nucleic acid (e.g. having sequence SEQ ID NO: 1, 23 or 24) under annealing conditions of low, moderate or high stringency conditions.

Please replace the paragraph at page 47, lines 7-19, as amended on January 27, 2004, with the following paragraph:

DNA sequence data produced from individual reactions were collected and the relative fluorescent peak intensities analyzed automatically on a PowerMAC computer using ABI Sequence Analysis Software (Perkin-Elmer). Individually autoanalyzed DNA sequences were edited manually for accuracy before being merged into a consensus sequence "string" using AutoAssembler software (Perkin-Elmer). Both strands of the HMW protein gene segment encoded by pAH306 were sequenced and these data

compiled to create a composite sequence for the HMW protein gene segment. The sequence encoding the segment of HMW protein is listed as SEQ ID No.: 10 and is represented by nucleotides 466 to 1976 in Figure 2A-C. A map of pAH306 is shown in Figure 5.

Please replace the paragraph at page 49, lines 19 to 21 with the following paragraph:

Plasmid pAH310 was one derivative isolated by these procedures and the coding segment of the HMW protein is represented by nucleotides 994-2401 in Figure 2A-C.

Please replace the paragraph at page 50, lines 3 to 15 as amended on January 27, 2004 with the following paragraph:

Plasmid pAH316 is one derivative isolated by these procedures. Restriction analysis of pAH316 demonstrated that this derivative contains a *C. trachomatis* L_2 insert of ~4.5 Kbp which consists of two EcoRI fragments of ~2.5 Kbp and ~2.0 Kbp in size. Southern hybridization analysis using the ~0.2 Kbp E/H fragment as a probe localized this sequence to the ~2.5 Kbp EcoRI fragment of pAH316. Directional PCR analyses employing purified pAH316 plasmid DNA as a template and amplification primer sets specific for ~0.2 Kbp E/H fragment and T3 and T7 vector sequences demonstrated pAH316 encodes the C-terminal segment of the HMW protein gene. The coding segment of the HMW protein is represented by nucleotides 1977 to 3420 in Figure 2A-C, and is listed as SEQ ID No.:11.

Please replace the paragraph at page 51, line 29 to page 52, line 7 as amended on January 27, 2004 with the following paragraph:

Mini-prep DNA from ampicillin-resistant transformants picked at random were prepared, digested to completion with XhoI, EcoRI, or a combination of both and examined for the presence and orientation of the ~1.5 Kbp truncated HMW protein ORF insert by agarose gel electrophoresis. Mini-prep DNA from clones determined to carry the ~1.5 Kbp XhoI/EcoRI insert was prepared and used to program asymmetric PCR DNA sequencing reactions to confirm the fidelity of the junction formed between the HMW protein fragment and the $(His)_6$ affinity purification domain of the expression vector. Plasmid pJJ36-J was one recombinant derivative isolated by these procedures and is represented by nucleotides 446 to 1980 in ~~figure 2~~ Figure 2A-C. The deduced amino acid sequence of the truncated fragment of HMW protein is represented by amino acids 29 to 533 in Figure 3 and is listed as SEQ ID No. 17.

Please replace the paragraph at page 56, lines 4-15, as amended on January 27, 2004 with the following paragraph:

DNA sequence data were collected using the ABI 310 Sequenator and analyzed automatically on a PowerMAC computer and appropriate computer software as described in Example 4. Individually autoanalyzed DNA sequences were edited manually for accuracy before being merged into a consensus sequence "string" using AutoAssembler software (Perkin-Elmer). Both strands of the HMW protein gene from the *C. trachomatis* B and F serovars were sequences for both the *C. trachomatis* B and F HMW protein genes. The amino acid sequences encoded are listed as SEQ ID Nos.: 15 and 16. Sequence comparisons of the L_2, F and B strains are presented in Figure 6A-B.

Please replace the paragraph at page 58, lines 6-18, as amended on January 27, 2004, with the following paragraph:

Mini-prep DNA from ampicillin-resistant transformants picked at random were prepared, digested to completion with KnI, HindIII, or a combination of both and examined for the presence and orientation of the ~3.2Kbp HMW protein ORF insert by agarose gel electrophoresis and ethidium bromide staining. Mini-prep DNA was used to program asymmetric PCR DNA sequencing reactions as described in example(s) above to confirm the fidelity of the junction formed between the HMW protein fragment and the $(His)_6$ affinity purification domain of the vector. Plasmid pAH342 was one derivative isolated by these procedures, which contains the HMW protein gene ORF from *C. trachomatis* L_2 and is represented by nucleotides 466 to 3421 in Figure 2A-C.

Please replace the paragraph at page 62, lines 24-36 with the following paragraph:

Identical cell samples stained with prebleed rabbit antibody or FITC-conjugated second antibody alone were processed in parallel and served as antibody specificity (negative) controls. Counterstained samples were examined at a 1000-X magnification with a Zeiss Axioskop photomicroscope equipped with plan-neoflur objectives. Results using *C. trachomatis* ~~N11~~ N11 (F serovar) are shown in Figure 7A-B. The results show that enhanced fluorescence of samples stained with HMW protein antibody compared to the controls confirmed the surface location of the HMW protein. Furthermore, fluorescence of samples stained with HMW protein antibodies show binding to surface localized HMW protein from L_2, B and MoPn serovars and *C. pneuomoniae*.